

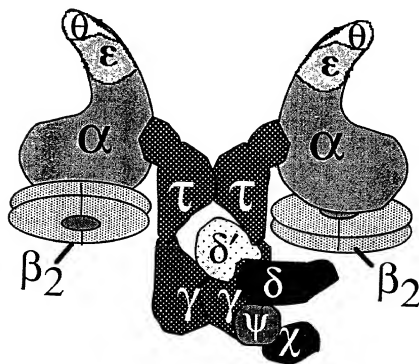
E. coli DNA Polymerase III

Figure 1

JCS002 U.S. PTO
09/642218
09/10/00

ATP binding

E. coli

MSYQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIH**HAYLFSGTRGVGKTS**IA RLLAK

B. subtilis

MSYQALYRVFRPQRFEDVVGQEHITKTLQNALLOKKF**SHAYLFSGPRGTGKTS**AAKIFAK

**** * * * * * . * * * . ***** * * * * * . **

E. coli

GLNCETGITATPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPARGRF

B. subtilis

AVNCEHAPVDEPCNECAACKGITNGSISDVIEIDAASNNGVDEIRDIRDKVKFAPSAVTY

.*** ** * * . * * . * .***** . . . * * . * . * . *

E. coli

KVYLIDEVHMLSRHSFNALL**KTLEEPPEH**VKFLATTDPOKLPVTILSRCLQFHLKALDV

B. subtilis

KVYIIDEVHMLSIGAFNALL**KTLEEPPEHC**IFILATTEPHKIPLTIISRCQRFDFKRITS

.** .***** * .***** . * . * . * . * . * . *

Figure 2

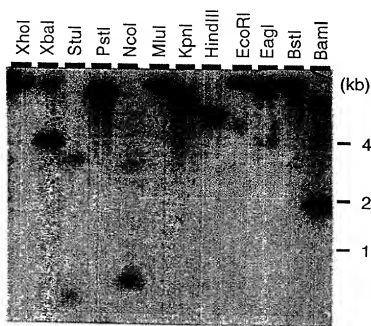


Figure 3

600-1-179 N (Sheet 4 of 31)

TCCGGGGGTG	GGGTTCCCAG	GTAGACCCCG	GCCCCCTCCG	TGAGCCCCCTT	TACCCAGGCC	60														
GCCACCTCCT	CCAGGGGGGC	CAAGGCGTGC	AAGGAGAGGA	ACGTCCGCAC	CAGCCC CTAT	120														
ACTAGCCTT	GTG met	AGC ser	GCC ala	CTC leu	TAC tyr	CGC arg	CGC arg	TTC phe	CGC arg	CCC pro	CTC leu	ACC thr	TTC phe	CAG gln	GAG glu	S.D. GTG val	GTG val	180 (17)		
GGG gly	CAG gln	GAG glu	CAC his	GTG val	AAG lys	GAG glu	CCC pro	CTC leu	CTC leu	AAG lys	GCC ala	ATC ile	CGG arg	GAG glu	GGG gly	AGG arg	CTC leu	GCC ala	^{CAC} CAG gln	240 (37)
<i>GCS</i> GCC	<i>TAC</i> TAC	<i>CTS</i> CTC	<i>TTC</i> TTC	<i>TCC</i> TCC	<i>GGG</i> GGG	<i>CCC</i> CCC	<i>AGG</i> AGG	<i>GGC</i> GGC	<i>GTG</i> GTG	<i>GGC</i> GGC	<i>AAG</i> AAG	<i>ACC</i> ACC	<i>ACC</i> ACC	<i>ACG</i> ACG	<i>GCG</i> GCG	<i>AGG</i> AGG	<i>CTC</i> CTC	<i>CTC</i> CTC	<i>GCC</i> GCC	300 (57)
ATG met	CGC ala	GTG val	GGG gly	TGC cys	CAG gln	GGG gly	GAA glu	CAC asp	CCC pro	CCT pro	TGC tyc	GGG gly	GTC val	TGC cys	CCC pro	CAC his	TGC cys	CAG gln	GCG ala	360 (77)
GTG Val	CAG gln	AGG arg	GGC gly	GCC ala	CAC his	CCG pro	GAC asp	GTG val	GTG val	GAC asp	ATT ile	GAC asp	GCC ala	GCC ala	AGC ser	AAC asn	AAC asn	TCC ser	GTG val	420 (97)
GAG glu	GAC asp	GTG val	CGG arg	GAG glu	CTG leu	AGG arg	GAA glu	AGG arg	ATC ile	CAC his	CTC leu	GCC ala	CCC pro	CTC leu	TCT ser	GCC ala	CCC pro	AGG arg	AAG lys	480 (117)
GTC Val	TTC phe	ATC ile	CTG leu	GAC asp	GAG Glu	GCC ala	CAC his	ATG met	CTC leu	TCC ser	AAA lys	AGC ser	GCC ala	TTC phe	AAC asn	GCC ala	CTC leu	CTC leu	^C AAG lys	540 (137)
<i>TGS</i> ACC	<i>CTS</i> CTG	<i>CTC</i> GAG	<i>CTC</i> glu	<i>GGG</i> glu	<i>GGG</i> pro	<i>CTC</i> pro	<i>GTG</i> pro	GTC his	CTC val	TTC leu	GTC phe	TTC val	GCC phe	ACC ala	ACC thr	GAG thr	CCC glu	GAG pro	AGG glu	600 (157)
ATG met	CCC pro	CCC pro	ACC thr	ATC ile	CTC leu	TCC ser	CGC arg	ACC thr	CAG gln	CAC his	TTC phe	CGC arg	TTC phe	CGC arg	CGC arg	CTC leu	ACG thr	GAG glu	GAG glu	660 (177)
GAG glu	ATC ile	GCC ala	TTT phe	AAG lys	CTC leu	CGG arg	CGC arg	ATC ile	CTG glu	GAG leu	GCC ala	GTG val	GGG gly	CGG arg	GAG glu	GCG ala	GAG glu	GAG glu	GAG glu	720 (197)
GCC ala	CTC leu	CTC leu	CTC leu	CTC leu	GCC ala	CGC arg	CTG leu	GCG ala	GAC asp	GGG gly	GCC ala	CTT leu	AGG arg	GAC asp	GCG ala	GAA glu	AGC ser	CTC leu	CTG leu	780 (217)
GAG glu	CGC arg	TTC phe	CTC leu	CTC leu	CTG leu	GAA glu	GGC gly	CCC pro	CTC leu	ACC thr	CGG arg	AAG lys	GAG glu	GTG val	GAG glu	CGC arg	GCC ala	CTA leu	GGC gly	840 (237)
TCC ser	CCC pro	CCA pro	GGG gly	ACC thr	GGG gly	GTG val	GCC arg	GAG ile	ATC ala	GCC ala	GCC ala	TCC ser	CTC leu	GCG arg	AGG gly	GGG arg	AAA lys	ACG thr	GCG ala	900 (257)
GAG glu	GCC ala	CTG leu	GGC gly	CTC leu	GCC ala	CGG arg	CGC arg	CTC leu	TAC tyr	GGG gly	GAA glu	GGG gly	TAC tyr	GCC ala	CCG pro	AGG arg	AGC ser	CTG leu	GTC val	960 (277)
TCG ser	GGC gly	CTT leu	TTG leu	GAG glu	GTG val	TTC phe	CGG arg	GAA glu	GGC gly	CTC leu	TAC tyr	GCC ala	GCC ala	TTC phe	GGC gly	CTC leu	GCG ala	GGA gly	ACC thr	1020 (297)
CCC pro	CTT leu	CCC pro	GCC ala	CCG pro	CCC gln	CAG ala	GCC met	CTG ile	ATC ala	GCC ala	GCC ala	ATG thr	ACC thr	GCC ala	CTG leu	GAC asp	GAG glu	GCC ala	ATG met	1080 (317)

Figure 4A

GAG CGC CTC GCC CGC CGC TCC GAC GCC TTA AGC CTG GAG GTG GCC CTC CTG GAG GCG GGA	1140
glu arg leu ala arg arg ser asp ala leu ser leu glu val ala leu leu glu ala gly	(337)
AGG GCC CTG GCC GCC GAG GCC CTA CCC CAG CCC ACG GGC GCT CCT TCC CCA GAG GTC GGC	1200
arg ala leu ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly	(357)
CCC AAG CCG GAA AGC CCC CCG ACC CCG GAA CCC CCA AGG CCC GAG GAG GCG CCC GAC CTG	1260
pro lys pro glu ser pro pro thr pro glu pro pro arg pro glu glu ala pro asp leu	(377)
CGG GAG CCG TGG CCG GCC TTC CTC GAG GCC CTC AGG CCC ACC CTA CCG GCC TTC GTG CCG	1320
arg glu arg trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg	(397)
GAG GCC CGC CCG GAG GTC CCG GAA GGC CAG CTC TGC CTC GCT TTC CCC GAG GAC AAG GCC	1380
glu ala arg pro glu val arg glu gly gln leu cys leu ala phe pro glu asp lys ala	(417)
TTC CAC TAC CGC AAG GCC TCG GAA CAG AAG GTG AGG CTC CTC CCC CTG GCC CAG GCC CAT	1440
phe his tyr arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his	(437)
frameshift site	
TTC GGG GTG GAG GAG GTC GTC CTC GTC CTG GAG GGA GAA AAA AAA AGC CTG AGC CCA AGG	1500
phe gly val glu glu val val leu val leu glu gly glu lys lys ser leu ser pro arg	(457)
CCC CGC CCG GCC CCA CCT CCT GAA GCG CCC GCA CCC CCG GGC CCT CCC GAG GAG GAG GTA	1560
pro arg pro ala pro pro pro glu ala pro ala pro gly pro pro glu glu glu val	(477)
GAG GCG GAG GAA GCG GCG GAG GAG GCC CCG GAG GAG GCC TTG AGG CCG GTG GTC CGC CTC	1620
glu ala glu glu ala ala glu glu ala pro glu glu ala leu arg arg val val arg leu	(497)
CTG GGG GGG CCG GTG CTC TGG GTG CCG CCG CCC AGG ACC CCG GAG GCG CCG GAG GAG GAA	1680
leu gly gly arg val leu trp val arg arg pro arg thr arg glu ala pro glu glu glu	(517)
CCC CTG AGC CAA GAC GAG ATA GGG GGT ACT GGT ATA TAA TGGGGGCATG ACGCGGACCAC	1740
pro leu ser gln asp glu ile gly gly thr gly ile *	(529)
CGACCTCGGA CAAGAGACCG TGGACAACAT CCTCAAGCGC CTCCGCCGTA TTGAGGGCCA	1820
GGTGCGGGGG CTCCAGAAGA TGGTGGCCGA GGGCCGCCCC TGCGACGAGG TCCTCACCCA	1880
GATGACCGCC ACCAAGAAGG CCATGGAGGC GCGGCCACC CTGATCCTCC ACGAGTTCCT	1940
GAACGTCTGC GCCGCCGAGG TCTCCGAGG CAAGGTGAAC CCCAAGAAGC CCGAGGAGAT	2000
CGCCACCATG CTGAAGAACT TCATCTA	2027

Figure 4B

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          GTG AGC GCC CTC TAC CGC CGC TTC CGC CCC CTC ACC TTC CAG GAG GTG GTG   51
GGG CAG GAG CAC GTG AAG GAG CCC CTC CTC AAG GCC ATC CGG GAG GGG AGG CTC GCC CAG   111
GCC TAC CTC TTC TCC GGG CCC AGG GGC GTG GGC AAG ACC ACC ACG GCG AGG CTC CTC GCC   171
ATG GCG GTG GGG TGC CAG GGG GAA GAC CCC CCT TGC GGG GTC TGC CCC CAC TGC CAG GCG   231
GtG CAG AGG GGC GCC CAC CCG GAC GTG GTG GAC ATT GAC GCC GCC AGC AAC AAC TCC GTG   291
GAG GAC GTG CGG GAG CTG AGG GAA AGG ATC CAC CTC GCC CCC CTC TCT GCC CCC AGG AAG   351
GTC TTC ATC CTG GAC GAG GCC CAC ATG CTC TCC AAA AGC GCC TTC AAC GCC CTC CTC AAG   411
ACC CTG GAG GAG CCC CCG CCC CAC GTC CTC TTC GTC TTC GCC ACC ACC GAG CCC GAG AGG   471
ATG CCC CCC ACC ATC CTC TCC CGC ACC CAG CAC TTC CGC TTC CGC CGC CTC ACG GAG GAG   531
GAG ATC GCC TTT AAG CTC CGG CGC ATC CTG GAG GCC GTG GGG CGG GAG GCG GAG GAG GAG   591
GCC CTC CTC CTC CTC GCC CGC CTG GCG GAC GGG GCC CTT AGG GAC GCG GAA AGC CTC CTG   651
GAG GCC CTG GGC CTC GCC CGG CGC CTC ACC CGG AAG GAG GTG GAG CGC GCC CTA GGC   711
TCC CCC CCA GGG ACC GGG GTG GCC GAG ATC GCC GCC TCC CTC GCG AGG GGG AAA ACG GCG   771
GAG GCC CTG GGC GCG GAG GGC CTC TAC GGG GAA GGG TAC GCC CCG AGG AGC CTG GTC   831
TCG GGC CTT TTG GAG GTG TTC CGG GAA GGC CTC TAC GCC GCC TTC GGC CTC GCG GGA ACC   891
CCC CTT CCC GCC CCG CCC CAG GCC CTG ATC GCC GCC ATG ACC GCC CTG GAC GAG GCC ATG   951
GAG GCG CTC GCC CCG CGC TCC GAC GCC TTA AGC CTG GAG GTG GCC CTC CTG GAG GCG GGA   1011
AGG GCC CTG GCC GCC GAG GCC CTA CCC CAG CCC ACG GGC GCT CCT TCC CCA GAG GTC GGC   1071
CCC AAG CCG GAA AGC CCC CCG ACC CCG GAA CCC CCA AGG CCC GAG GAG GCG CCC GAC CTG   1131
CGG GAG CCG TGG CCG GCC TTC CTC GAG GCC CTC AGG CCC ACC CTA CGG GCC TTC GTG CCG   1191
TTC CAC TAC CCG AAG SCC TCG GAA CAG AAG GTG AGG CTC CTC CCC CTG GCC CAG GCC CAT   1251
GAG GCC CCG GCC CCA CCT CCT GAA GCG CCC GCA CCC CCG GGC CCT CCC GAG GAG GAG GTA   1311
GAG GCG GAG GAA GCG GCG GAG GAG GCC CCG GAG GAG GCC TTG AGG CGG GTG GTC CGC CTC   1371
CTG GGG GGG CCG GTG CTC TGG GTG CCG CCG ACC AGG ACC CGG GAG GCG CCG GAG GAG GAA   1431
          CCC CTG AGC CAA GAC GAG ATA GGG GGT ACT GGT ATA TAA   (1590)

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Figure 4C

Met ser ala leu tyr arg arg phe arg pro leu thr phe gln glu val val gly gln glu 20
 his val lys glu pro leu leu lys ala ile arg glu gly arg leu ala gln ala tyr leu 40
 phe ser gly pro arg gly val gly lys thr thr thr ala arg leu leu ala met ala val 60
 gly cys gln gly glu asp pro pro cys gly val cys pro his cys gln ala val gln arg 80
 gly ala his pro asp val val asp ile asp ala ala ser asn asn ser val glu asp val 100
 arg glu leu arg glu arg ile his leu ala pro leu ser ala pro arg lys val phe ile 120
 leu asp glu ala his met leu ser lys ser ala phe asn ala leu leu lys thr leu glu 140
 glu pro pro pro his val leu phe val phe ala thr thr glu pro glu arg met pro pro 160
 thr ile leu ser arg thr gln his phe arg phe arg arg leu thr glu glu glu ile ala 180
 phe lys leu arg arg ile leu glu ala val gly arg glu ala glu glu glu ala leu leu 200
 leu leu ala arg leu ala asp gly ala leu arg asp ala glu ser leu leu glu arg phe 220
 leu leu leu glu gly pro leu thr arg lys glu val glu arg ala leu gly ser pro pro 240
 gly thr gly val ala glu ile ala ala ser leu ala arg gly lys thr ala glu ala leu 260
 gly leu ala arg arg leu tyr gly glu gly tyr ala pro arg ser leu val ser gly leu 280
 leu glu val phe arg glu gly leu tyr ala ala phe gly leu ala gly thr pro leu pro 300
 ala pro pro gln ala leu ile ala ala met thr ala leu asp glu ala met glu arg leu 320
 ala arg arg ser asp ala leu ser leu glu val ala leu leu glu ala gly arg ala leu 340
 ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly pro lys pro 360
 glu ser pro pro thr pro glu pro pro arg pro glu glu ala pro asp leu arg glu arg 380
 trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg glu ala arg 400
 pro glu val arg glu gly gln leu cys leu ala phe pro glu asp lys ala phe his tyr 420
 arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his phe gly val 440
 glu glu val val leu val leu glu gly glu lys lys ser leu ser pro arg pro arg pro 460
 ala pro pro pro glu ala pro ala pro pro gly pro pro glu glu glu val glu ala glu 480
 glu ala ala glu ala pro glu glu ala leu arg arg val val arg leu leu gly gly 500
 arg val leu trp val arg arg pro arg thr arg glu ala pro glu glu glu pro leu ser 520
 gln asp glu ile gly gly thr gly ile 529

Figure 4D

Met ser ala leu tyr arg arg phe arg pro leu thr phe gln glu val val gly gln glu 20
 his val lys glu pro leu leu lys ala ile arg glu gly arg leu ala gln ala tyr leu 40
 phe ser gly pro arg gly val gly lys thr thr thr ala arg leu leu ala met ala val 60
 gly cys gln gly glu asp pro pro cys gly val cys pro his cys gln ala val gln arg 80
 gly ala his pro asp val val asp ile asp ala ala ser asn asn ser val glu asp val 100
 arg glu leu arg glu arg ile his leu ala pro leu ser ala pro arg lys val phe ile 120
 leu asp glu ala his met leu ser lys ser ala phe asn ala leu leu lys thr leu glu 140
 glu pro pro pro his val leu phe val phe ala thr thr glu pro glu arg met pro pro 160
 thr ile leu ser arg thr gln his phe arg phe arg arg leu thr glu glu glu ile ala 180
 phe lys leu arg arg ile leu glu ala val gly arg glu ala glu glu glu ala leu leu 200
 leu leu ala arg leu ala asp gly ala leu arg asp ala glu ser leu leu glu arg phe 220
 leu leu leu glu gly pro leu thr arg lys glu val glu arg ala leu gly ser pro pro 240
 gly thr gly val ala glu ile ala ala ser leu ala arg gly lys thr ala glu ala leu 260
 gly leu ala arg arg leu tyr gly glu gly tyr ala pro arg ser leu val ser gly leu 280
 leu glu val phe arg glu gly leu tyr ala ala phe gly leu ala gly thr pro leu pro 300
 ala pro pro gln ala leu ile ala ala met thr ala leu asp glu ala met glu arg leu 320
 ala arg arg ser asp ala leu ser leu glu val ala leu leu glu ala gly arg ala leu 340
 ala ala glu ala leu pro gln pro thr gly ala pro ser pro glu val gly pro lys pro 360
 glu ser pro pro thr pro glu pro pro arg pro glu glu ala pro asp leu arg glu arg 380
 trp arg ala phe leu glu ala leu arg pro thr leu arg ala phe val arg glu ala arg 400
 pro glu val arg glu gly gln leu cys leu ala phe pro glu asp lys ala phe his tyr 420
 arg lys ala ser glu gln lys val arg leu leu pro leu ala gln ala his phe gly val 440
 glu glu val val leu val leu glu gly glu lys lys lys pro asp pro lys ala pro pro 460
 gly pro thr ser 464

Figure 4E

Met	ser	ala	leu	tyr	arg	arg	phe	arg	pro	leu	thr	phe	gln	glu	val	val	gly	gln	glu	20
his	val	lys	glu	pro	leu	leu	lys	ala	ile	arg	glu	gly	arg	leu	ala	gln	ala	tyr	leu	40
phe	ser	gly	pro	arg	gly	val	gly	lys	thr	thr	thr	ala	arg	leu	leu	ala	met	ala	val	60
gly	cys	gln	gly	glu	asp	pro	pro	cys	gly	val	cys	pro	his	cys	gln	ala	val	gln	arg	80
gly	ala	his	pro	asp	val	val	asp	ile	asp	ala	ala	ser	asn	asn	ser	val	glu	asp	val	100
arg	glu	leu	arg	glu	arg	ile	his	leu	ala	pro	leu	ser	ala	pro	arg	lys	val	phe	ile	120
leu	asp	glu	ala	his	met	leu	ser	lys	ser	ala	phe	asn	ala	leu	leu	lys	thr	leu	glu	140
glu	pro	pro	pro	his	val	leu	phe	val	phe	ala	thr	thr	glu	pro	glu	arg	met	pro	pro	160
thr	ile	leu	ser	arg	thr	gln	his	phe	arg	phe	arg	arg	leu	thr	glu	glu	glu	ile	ala	180
phe	lys	leu	arg	arg	ile	leu	glu	ala	val	gly	arg	glu	ala	glu	glu	glu	ala	leu	leu	200
leu	leu	ala	arg	leu	ala	asp	gly	ala	leu	arg	asp	ala	glu	ser	leu	leu	glu	arg	phe	220
leu	leu	leu	glu	gly	pro	leu	thr	arg	lys	glu	val	glu	arg	ala	leu	gly	ser	pro	pro	240
gly	thr	gly	val	ala	glu	ile	ala	ala	ser	leu	ala	arg	gly	lys	thr	ala	glu	ala	leu	260
gly	leu	ala	arg	arg	leu	tyr	gly	glu	gly	tyr	ala	pro	arg	ser	leu	val	ser	gly	leu	280
leu	glu	val	phe	arg	glu	gly	leu	tyr	ala	ala	phe	gly	leu	ala	gly	thr	pro	leu	pro	300
ala	pro	pro	gln	ala	leu	ile	ala	ala	met	thr	ala	leu	asp	glu	ala	met	glu	arg	leu	320
ala	arg	arg	ser	asp	ala	leu	ser	leu	glu	val	ala	leu	leu	glu	ala	gly	arg	ala	leu	340
ala	ala	glu	ala	leu	pro	gln	pro	thr	gly	ala	pro	ser	pro	glu	val	gly	pro	lys	pro	360
glu	ser	pro	pro	thr	pro	glu	pro	pro	arg	pro	glu	glu	ala	pro	asp	leu	arg	glu	arg	380
trp	arg	ala	phe	leu	glu	ala	leu	arg	pro	thr	leu	arg	ala	phe	val	arg	glu	ala	arg	400
pro	glu	val	arg	glu	gly	gln	leu	cys	leu	ala	phe	pro	glu	asp	lys	ala	phe	his	tyr	420
arg	lys	ala	ser	glu	gln	lys	val	arg	leu	leu	pro	leu	ala	gln	ala	his	phe	gly	val	440
glu	glu	val	val	leu	val	leu	glu	gly	glu	lys	lys	lys	ala							454

Figure 4F

		ATP site	
E.coli	MSYQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIHHAYLFS	SGTRGVGKTSIARLLAK	60
H.inf.K.....II.....KDN.L.....F..	60
B.sub.	...A.Y.VF...R.E.....ITKT.Q.A.LQKFS.....	P.T...A.KIF..	60
C.cres.	DA.T...Y..R..E.LI...AMVRT...AF.T...A..FMLT.V.....	TT...R	113
M.gen.	-MH..FYQ.Y..IN.KQTL...SIRKI.V.AINRDKLPNG.I...E.T...TF.KII..		59
T.th.	--VSA.Y.RF..L..QE.....KEP.LKAIRE..LAQ.....P.....TT.....	M	58
Zn ²⁺ finger			
	* * *		
E.coli	GLNCET---GITATPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPA		116
H.inf.	...VH---V.....E.E..KA...N.I.....E.....K.V	116
B.sub.	AV...H---APVDE..NE.AA.KG.TN.SIS.V.....	NNG.DEI..IR.K.KP..S	116
C.cres.	A..Y..DTVK.PSVDLTTTEGYH..S.IE..HM.VL.L.....	DEM.E...G.R...V	173
M.gen.	AI..LN---WDQIDV.NS..V.KS.NTNSAI.IV.....	KNGIN.I.E.VE..FNH.F	115
T.th.	AVG.QG-----EDP.....PH.QAVQR.AHP.VVD.....	NNS...V.E.RERIH.L	112
E.coli	RGRFVKYLIDEVHMLSRHSFNALKLTLEEPPEHVKFLLATDPQKLPVTILSRCLQPHLK		176
H.inf.	V.....Y.....	176
B.sub.	AVTY...I.....IGA.....	CI.I...E.H.I.L..I...QR.DF.	176
C.cres.	EA.Y...I.....TAA.....	P.A..IF...EIR.V.....QR.D.R	233
M.gen.	TFKK...IL..A...TTQ.WGG.....	S.PY.L.IFT..EFN.I.L.....QS.FF.	175
T.th.	SAPR..FIL..A...KSA.....	P..L.VF...E.ERM.P.....TQH.RFR	172
E.coli	ALDVEQIRHQLEHILNEEHIAHEPRALQLLARAEGSLRDALSLTDQAIASGDGQ--VST		234
H.inf.	...EQ..SQH.A...TQ.N.PF.DP..VK..K..Q..I..S.....	M.R.--TN	234
B.sub.	RITSQA.VGRMNK.VDA.QLQV.EGS.EII.S..H.GM.....	L...SFSGDI--LKV	234
C.cres.	RVEPDVLVKHFD.R.SAK.GARI.MD..A.I.....	V..G...L...VQTERGQT.TS	293
M.gen.	KITSDL.LER.ND.AKK.K.KI.KD..IKI.DLSQ.....	G...L..LAI.LIVKKL.LL	235
T.th.	R.TE.E.AFK.RR..EAVGRE.A.EE..L....L.D.A....E..LERFLLLEGP--LTR		229
E.coli	QAVSAMLGTLDDDDQALSIVEAMVEANGERVMA LINEAAARGIEWEALLVEMGLLHRIAM		294
H.inf.	NV..N...L...NYSVDILY.LHQG...LL.RTLQRV.DAAGD.DK..G.CAEK..Q..L		294
B.sub.	EDALLIT.AVSQLYIGK.AKSLHDK.VSDALETI..LLQQ.KDPK.IED.IFYFRDMLL		294
C.cres.	TV.RD...LA.RS.TIA.Y.HVMAGTKDALEGFRALWGF.ADPAPVMLDV.DHC.AS.V		353
M.gen.	MLKKHLISLIEMQNL.L.KQFYQ.I		260
T.th.	KE.ERA..SPPGTGVAETIAASLARGKTAEALG.ARRLYGE.YAPRS.VSGL.EVPFREGLY		289

Figure 5

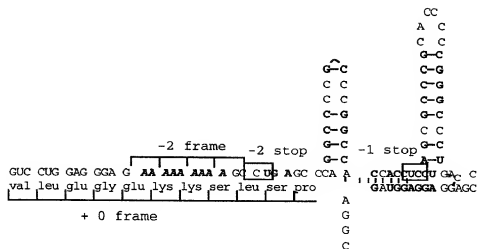


Figure 6

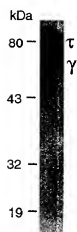
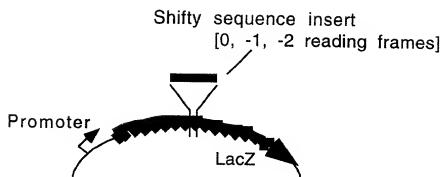


Figure 7



	Reading frame	Blue	White
Shifty sequence	0	+	
	- 1	+	
	- 2	+	
Mutant sequence	0	++	
	- 1		+
	- 2		+

Figure 8

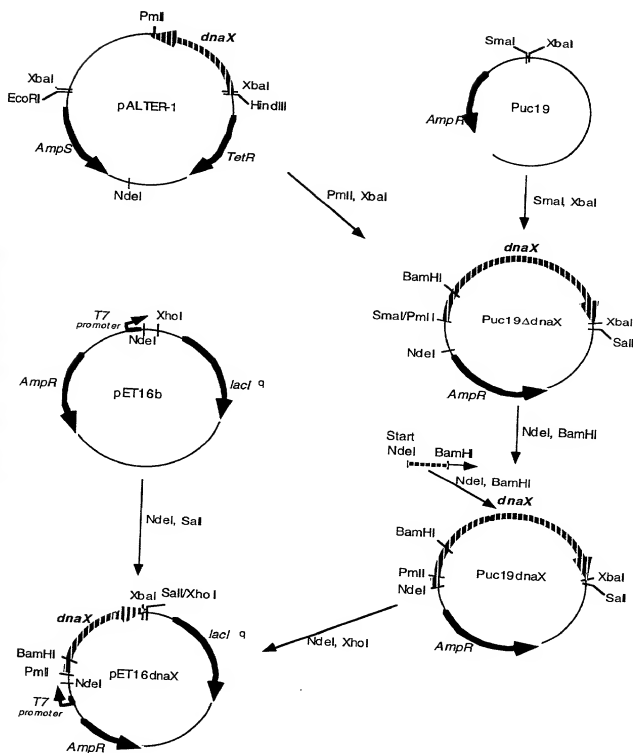


Figure 9

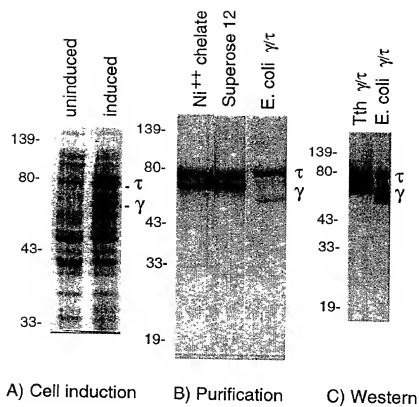


Figure 10

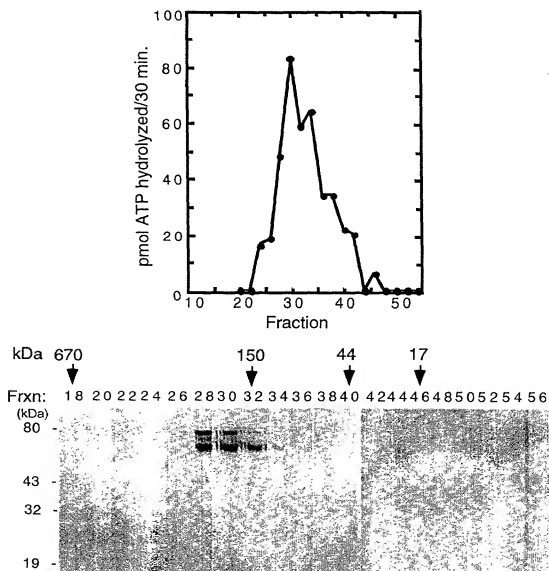


Figure 11

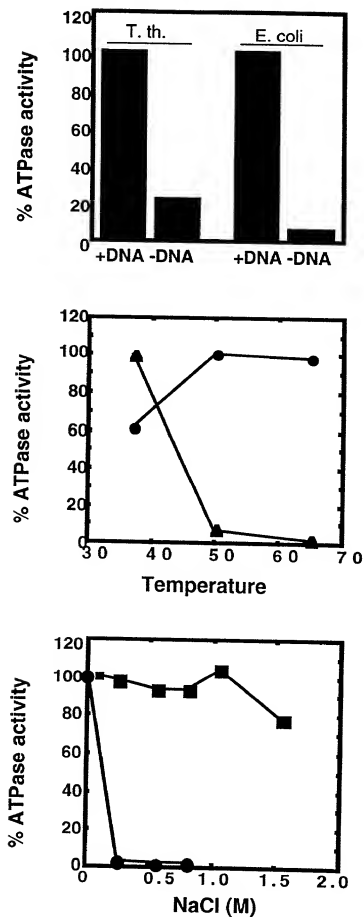
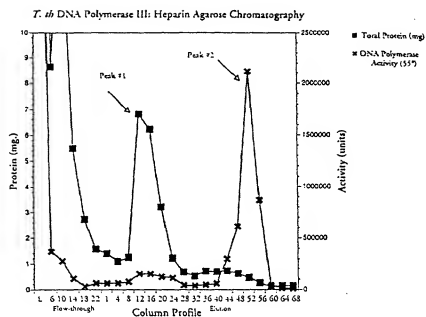


Figure 12

A)



B) ATP Agarose Step Column

C)

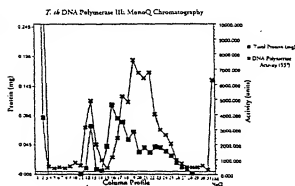
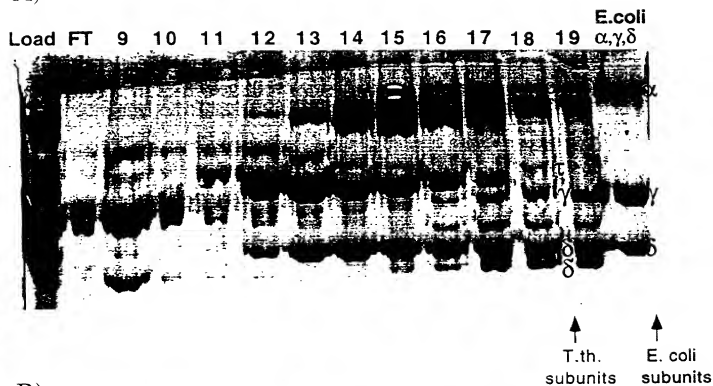


Figure 13

A)



B)

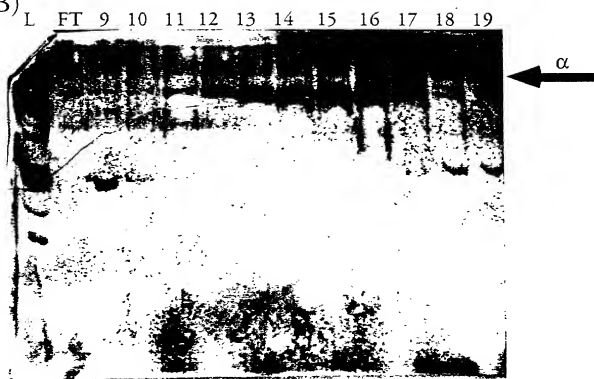


Figure 14

A) Alignment of TTH1 with alphas subunits of other organisms.

E.coli	DRYFLELIRTGRPDEESYLHAAVELAEARGLPVV	197	(ID#72)
V.chol.	DHFYLELIRTGRADEESYLHFALDVAEQYDLPVV	197	(ID#73)
H.inf.	DHFYLALSRTRGRPEERYIQAAKLAEACDLPLV	197	(ID#74)
R.prow.	DRFYFEIMRHDLPPEEQFIENSYIQIASELSIPIV	195	(ID#75)
H.pyl.	DDFYLEIMRHGILDQRFIDEQVIKMSLETGLIKII	213	(ID#76)
S.sp.	DDYYLEIQDHGSVEDRLVNINLVKIAQELDIKIV	202	(ID#77)
M.tub.	DNYFLELMDHGLTIERRVRDGLLEIGRALNIPPL	220	(ID#78)
T.th.	FFIEIQNHGLSEQK		(ID#61)

B) Alignment of TTH2 with alphas subunits of other organisms.

E.coli	NKRRAKNGEPPLDIAAIPLDDKKSFDMLQRSETTAVFQLESRGMKD	618	(ID#79)
V.chol.	NPRLLKAGKGPVRIEATPLDDARSFRNLQDAKTTAVFQLESRGMKD	618	(ID#80)
H.inf.	NVRMVRGKGRPRVDIAAIPLDDPESFELLKRSETTAVFQLESRGMKD	618	(ID#81)
R.prow.	CKKLLKEQGIKIDFDDMTFDDKKTYQMLCKGKGVGVQFESIGMKD	624	(ID#82)
H.pyl.	LKIIKTQHKISVDFSLDMDDPKVYKTIQSGDTVGIFQIES-GMFQ	648	(ID#83)
S.sp.	QERKALQIRARTGSKKLPDDVKKTHKLEAGDLEGIFQLESQGMKQ	643	(ID#84)
M.tub.	IDNVRANRGIDLDLESVPPLDDKATYELLGRGDTLGVFQLDGGPMRD	646	(ID#85)
T.th.	RVELDYDALTLDD		(ID#60)

Figure 15

A)

Start codon

ATGGGCGGGAGCTCCGCTTCGCCCCACCTCCACCAGCAC
 CCCAGTTCTCCCTCCTGGACGGGGCGCGAAGCTTTCCGA
 CCTCCTCAAGTGGGTGGAGGAGACGACCCCGAGGACCCC 120
 GCCTTGGCCATGACCGACCACGGCAACCTCTTCGGGGCCG
 TAGAGTTCTACAAGAAGGCCGCCGAAATGGGCATCGAGCC
 CATCCTGGGTACGAGGCCTTACGTGGCGCGGAAAGCCG 240
 TTTGACCGCAAGCGGGGAAAGGGCTAGACGGGGGTACT
 TTCACCTCACCTCCTCGCGCAAGGACTTACGGGGTACCA
 GAACCTGGTGCCTCGCGAGCGGGCTTACCTGGAGGGG 360
 TTTTACGAAAAGCCCGGATTGACGGGAGATCTCGCGG
 AGCGCCGAGGGCCTCATCGCCTCTCGGGGTGCCTCGGGG
 GGAGATCCCCAGTTTCATCTCCAGGACCGTCTGGAGCTG 480
 GCGAGGGCCGGCTCAACGAGGACCTCTCCATCTTCAAGG
 ACCGCTTCTTCATTCACATCCAGAACCCAGCGCTCCCCGA
 GCAGAAAAAGGTCAACGAGGTCTCTAAGGAGTTCGCCCGA 600
 AAGTACGGCTGGGGATGGTGGCCACCAACGACGGCCATT
 ACGGGAGGAAGGAGGCCCGCAGCGCCACGAGGTTTTCCT
 CGCCATCTCAGTCCAAGAGCACCTTGGACGACCCGGGGCC 720
 GTTGGCTTTCCCTGCGGGAGTTTACGTGAAGACCCCG
 AGGAGACGTGCGGGCCGGTGTTCCTCCGAGGAGGAGTGGG
 GGACGAGCCCTTTGACAACCCGTGGAGATCGCCCCGATG 840
 TGCAACCTGGAGCTGCCCATCGGGACAAGATGGTCTACCC
 GAATCCCCCGCTTCCCCCTCCCGGAGGACCGGGGACCGA
 GGCCAAAGTACCTAATGGAGCTAACCTTCAAGGGGCCCTC 960
 CGCGTTTACCGGACCGAATACCGAGGGTTTCTACCGGG
 AGGTTTTCGGCTTTTGGGGAAGCTTCCCCCCCACGGGCA
 CGGGGAGGCCTTGGCCGAGGCTTGGCCAGGTGGAGCGG 1080
 GAGGCTTGGGAGAGGCTCATGAAGAGCCTCCCCCCCCTTG
 ACCGGGGTCCAAGGAGTTCCA

B)

MGRELRFALHGHQHTQFSLLDGAPKLSDLLKWEETTPEDP
 ALAMTDHGNLFGAVEFYKKAEMGIEPIIGTRPYVAESP
 FDRKRGKGLDGGYFHLTLAKDFTGYQNLVRLASRAYLEG 120
 FYEKPRIDREILRERRRPHRLSGCLGAIEIPQFILQDRLLD
FFIEIQNHGLSEQK
 AEARNLEDLSIFKDRFFIHIQNHGLPEQKKVNEVLKEFAR
 KYGLGMVATNDGHYGRKEARSAHEVFLAIQSKSTLDDPGA 240
 VGFPLREFYVKTPEETCGVPFEEEWGDEPFDNTVEIARM
 CNVELPIGTRWSTRIPRFPLPEGPGTEAKYLMELTFKGPL
 RRYPRDRIEGFYREVFRLLGKLPHPHGEALAEALQVER 360
 EAWERLMKSLPPFDRGPRSS

Figure 16

	Start1	Start2	3'-Exo I
T. th.	VERVVRTLLDGRFLEEGLWEWRYPPFLEGEAVVVL DLETT GLAG-----LDEVIEVGLLRLEGG---RRLPF		
D. rad.		PWPQDVVV FDETT GFSPA-----SAAIVEIGAVRIVGGQIDETLKF	
Bac. sub.	HGIKMIYGMEANLVDDGVPIAYNAHRLLLEET YVVFDETT GLSAV-----YDTIIELAAVKVKGGE--IIDKF		
H. inf.		MINPNR QIVLDETT GMNQLGAHYEGHCIIIEIGAVELINRR--YTGNX	
E. c.		MSTAITR QIVLDETT GMNQLGAHSEGHKIIIEIGAVEVNNRR--LTGNF	
H. pyl.	NLEYLKACGLNFIETSENILITLKNLTKPLKDEV FSFIDLETT GCSCI-----KHEILEIGAVQVKGGE--IINRF		

	3'-Exo II
T. th.	QSLVR-PLPP---AEARSWNLT---GIPREALEEAPSLEEVELEKAYPLRGDATL VIHNAAFDLGFL -RPALEGLG
D. rad.	ETLVR-PTRPDGSMLSIPWQAQRVHGISEDEMVRAPAKDVLPDFDFVDGS AVAHNVSFDDGFM -RAGAERLG
Bac. sub.	EAFAN-PHRP---LSATIIELT---GITDDMLQDAPDVVDVIRDREWIGDDIL VAHNASFDMGFL -NVAYKKLL
H. inf.	HIYIK-PDRP---XDPDAIKVH---GITDEMLADKPEFKEVAQDFLDVINGAELL LIHNAFFDVGFM -DYEFRKLN
E. c.	HVYLK-DRLV---DPEAFGVH---GIAVDFLDKPTFAEVAVEFMDYIRGAEL VIHNAAFDVGFM -DYEFSLLK
H. pyl.	ETLVKVKVSP---DYIAELT---GITYEDTLNAPSAAHEALQELRLFLGNSVF VAHNAFDYNFL GRYFVEKLH

	3'-Exo IIIC
T. th.	-----YRLNPVVDLSRLARRGLPGLRRYGLDALSEVLELPRRT--- CHRALEDVERTLAVVHEVYYMLT -----SG
D. rad.	-----LSWAPERELCTMQLSRAFPRETRHNTLVLAERLGLFAPGGR HRSYGDVQVTAQAYLRLELLG -----ER
Bac. sub.	E---VEKAKNPVIDTLELGRFLYPEFKNHLNTLCKKFDIELTQ--- HHRAIYDTEATAYLLKMLKDA -----EK
H. inf.	-LNVKTDDICLVDTTLQMARQMPGKRN-MLDALCDRLGIDNSKRTL HGALLDAEILADVYLMMTGGQTNLFDEEE
E. c.	RDIAKTNTFCVKVDSLAVARKMPGKRN-SLDALCARYEIDNSKRTL HGALLDAQILA EVYLA MTGGQTSMAFAME
H. pyl.	-----CPLNLNKLCTLDLSKRAILSMRY-SLSFLKELLGFGIEV--- SHRAYADALASYKLF EICLLNLP--SYIKT

Figure 17

A)

ATGGTGGAGCGGGTGGTGC GGACCTTCTGGACGGGAGGT 40
 TCCTCCTGGAGGAGGGGGTGGGGCTTGGGAGTGCGCTA
 CCCCTTTCCTGGAGGGGGAGGCGGTGGTGGTCTCTGGAC 120
 CTGGAGACCA CGGGCTTCCGGCCTGGACGAGGTGATTG
 AGGTGGGCCTCTCCGCCTGGAGGGGGGAGGCGCCTCCC 200
 CTTCAGAGCCTCGTCCGGCCCTCCCGCCCGCGAAGCC
 CGTTCGTGGAACCTCACCGGCATCCCCGGGAGGCGCTGG 280
 AGGAGGCCCCCTCCCTGGAGGAGGTTCTGGAGAAGGCCTA
 CCCCCTCGCGCGGACGCGACCTTGGTGATCTACAACGCC 360
 GCCTTTGACCTGGGCTTCCTCCGCGGGCCTTGAGGGCC
 TGGGCTACCGCCTGGAAAACCCCGTGGTGGACTCCCTGCG 440
 CTTGGCCAGACGGGGCTTACAGGCCTTAGGCGCTACGGC
 CTGGACGCCCTCTCCGAGGTCCTGGAGCTTCCCCGAAGGA 520
 CCTGCCACCGGGCCCTCGAGGACGTGGAGCGCACCCCTCGC
 CGTGGTGACGAGGTATATACTATGCTTACGTCCGGCCGT 600
 CCCCACGCTTTGGGAAC TCGGAGGTAG

B)

MVERVVRTLLDGRFLLEEGVGLWEWRYPPFLEGEAVVVLD 40
 LETTGLAGLDEVIEVGLRLRLECGRRLPFQSLVRPLPPAEA
 RSWNLTGIPREALEEAPSLEEVLKAYPLRGDATLVIHNA 120
 AFDLFLRPALEGLGYRLNFPVDSLRLARRGLPGLRRYG
 LDALSEVLELPRRTCHRALEDVERTLAVVHEVYYMLTSGR 200
 PRTLWELGRZ

Figure 18

Alignment of dnaA genes.

P. mar.	MLEASWEK	VQSSL--KQNLK--	-----PSYE	TWIRPTFESG--FKN	GELTLIAPNSFSSAW	LKNYYSQIQTBAE--	65
Syn. sp.	MVSCENLWQ	AAAIL--ATQLTK--	-----PAFD	TWIKASVLIS--LGD	GVATIQVENGVLNH	LQSYSGPLMEVLTV	67
B. sut.	MENILDLWQ	ALAQI--EKKLK--	-----PSFE	TWMKSTKAHS--LQG	DILTITAPNEFARDW	LESRYHLIADITY--	67
M. tub.	MTDDPGSGFTTVMNA	VVSELGNDPKVDDGP	SSDANLAPLTPQQR	AWLNLVQPLT--IVE	GALLSLVSPSSFQONE	IERHLRAPITDALS--	87
T. th.	MSHEAVWQH	VLEHI--RRSTIE--	-----VEFH	TWFERIRPLG--IRD	GULELAVPTSFALDW	IRRHVAGLIQBGPR--	66
E. coli	MSLSLWQ	CLARL--QDELPA--	-----TEFS	MTWIRPLQAE--LSD	NTLALYAPNRFVLDW	VRDKYLNININGLIT--	64
T. mar.	MKER	ILQEI--KTRVNR--	-----KSWE	LWFSFSDVKS--IEG	NKVVSVGNLFKSW	LEKYYSVLSKAVK--	61
H. pyl.	MDTNNIEKE	ILALVKQNPVSL--	-----IEYE	NYFSQLKYNPNAKS	DIAFFAPNQVLCTT	ITAKYGALLKEILSQ	72
P. mar.	EIFG---EPVTVMK	VKANASSDEHYSSA	P-----	---ITPPLASPGSV	DSSGSSLRSLK----	-KTLPLNLRYVFNH	130
Syn. sp.	DLTG---QKITVKLI	TGDLPHS---LIQO	E-----	---SSLPMETTP--	-----	-KNATALNGKYTFSR	115
B. sut.	ELTG---EELSIFKV	IPQNVQVEDFMPKPQ	VKKAVKEDTSDFQCN	-----	-----	---MLNPKYTFDT	119
M. tub.	RRIGH-QIQLGVRIA	PPATDEADDTVPVPS	ENPATISPTDTTND	EIDDSAAARGDNQHS	WPSYFTEPHTDGA	TAGVTLNLNRYTFT	176
T. th.	LLGAQ-APRFELRVV	PGVVVEDIFQPPPS	PPAQAP--	-----	-----	---EDTFKT	108
E. coli	SFGADAPQLRFEVG	TKPTVITPQAQVTSN	VAAAPQAQVTPQRA	APSTRSGWLNVPAPA	EP-----	-TYRSNNVNGHTFDN	140
T. mar.	VVLG---NDATFEIT	YEAFEPHSSSYEPLV	KKRAVLLTP--	-----	-----	---LNDPTTFEN	106
H. pyl.	NKVG-MHLAHSVDVR	IEVAPKIQINAQSN	NYKAIKTS-----	-----	-----	---VKDSTTFEN	118
P. mar.	FVVGPNRMAHAAM	AVAESGPREFNPLFI	CGGVGLGKTHLMQAI	GHYRLIDPGAKVSY	VSTETFINDLIL--A	IRQDMQAFDRDVR--	217
Syn. sp.	FVVGPNRMAHAASL	AVAESGPREFNPLFI	CGGVGLGKTHLMQAI	AHYRLMEYPAKVSY	VSTERFTNDLIT--A	IRQDNMEDFRSYR--	202
B. sut.	FVVGPNRMAHAASL	AVAESAAPKYNPLFI	CGGVGLGKTHLMHAI	GHYVIDHNPASKVSY	LSSEKTFNEFIN--S	IRDNKAVDFNRNRY--	206
M. tub.	FVVGPNRMAHAASL	AVAESAAPKYNPLFI	WGESGLGKTHLHAA	GNVQRLFPQMRKVY	VSTEEFTNDFIN--S	LRDDKAVFKRYSR--	263
T. th.	SWGPTTFWTHGAV	AAEAESGRAYNPLFI	YGGRLGKTYLTHHAV	GLPRAKRFPHMLRY	VSTETFTNELINRPS	AR-DMTEPRERYR--	196
E. coli	FVEKGNQARAARAR	QVANGHGRAYNPLFI	YGGTGLGKTHLHAA	GNGLMARKNPKVSY	MHSERFQDMVK--A	LQNNAIIEEFKRYR--	227
T. mar.	FVVGPNRMAHAAL	EAVKHGR--YNPLFI	YGGVGLGKTHLQSI	GNVYVQNEPLRVMY	VTSEFLNDLVD--S	MKEGKLNEFEKRYK	193
H. pyl.	FVVGSCNMTVYEIAK	KVAQSDTPPNYPLVF	YGGTGLGKTHLNAI	GNHAALEK--HKKVVL	VTSEDFLTDFLK--H	LDNRKMDSPKAKYR--	203
P. mar.	AADLILVDDIQPIEG	KEYTOEEFFHTFNAL	HDAGSQIVLASDRPP	SQIPRIQERLMSRPS	MGLIADVQAPDLETR	MAILQKKAHEHVRGL	307
Syn. sp.	SADFLIIDDIQPIKG	KEYTOEEFFHTFNAL	HEAGKQVWVASSDRAP	QRIPGLQRLISRPS	MGLIADIQVDPLETR	MAILQKKAERYDRL	292
B. sut.	NVDVLIIDDIQPIAG	KEYTOEEFFHTFNAL	HEESKQIVISSDRPP	KEIPTLEDRLSRFE	MGLITDITPPDLETR	IAILRKKAKBAGDIL	296
M. tub.	VVDVLIIDDIQPIEG	KEYTOEEFFHTFNAL	HNANKQIVISSDRPP	QOLATLEDRLSRFE	MGLITDVPQPELETR	IAILRKKAKBAGDIL	353
T. th.	SVDLLIIDDIQPIAG	KEYTOEEFFHTFNAL	YEAHQIILSSDRPP	KDILLLEARLSRFE	MGLITNDAPDLETR	IAILRKKAS--SPGED	285
E. coli	SVDALLIIDDIQFFAN	KERSQOEEFFHTFNAL	LEGNQOILTSDRVP	KEINGVEDRLSRFG	MGLTVAIEPPELETR	VAIIMKKADENDRL	317
T. mar.	KVDLILIIDDVQLIG	KYGQVTELEFHTFNEL	HDGSKQIVICSDRPP	QKLSSEFQRLSRKFE	MGLVAKLEPPDESTR	KSLVAKLEPHEGEL	283
H. pyl.	HCDFEFLDDAQFLOG	KPKLEEFFHTFNEL	HANSKQIVLISDRSP	KNIAGLEDRLSRFE	WGITAKVMPDLETR	LSIVRQKQQLNQITL	293
P. mar.	PRDLIOFIAGRFTSN	IRELEGALTRAIATA	SITGLPMTVDSIARM	LD-----PNQGVQVET	PQKVLKVAEYFKVT	PDEMRASRRR--FVS	392
Syn. sp.	PKEVIEYIAHSTNVS	IRELEGALTRAIATV	SLSNVMTVENIAPV	LN-----PPVEKVA	PETITIVIAQHYQNLK	VEELLNSRRR--EVS	377
B. sut.	PNEVMYIATNQIDSN	IRELEGALTRIVVYS	SLINKDNADLAABA	LKDII--FESKPVIT	IREKQVQVQGFNKL	LEDFKAKKRTK--SVA	384
M. tub.	PDDVLELJASSIERN	IRELEGALTRIVATA	SLAKPTIDKALAEIV	LRDLI--ADANTMTQS	ANTIMTAASYFDIT	VELLGRPGKTR--ALA	441
T. th.	PEDALEYIARQVTSN	IREWEGALMRASPIA	SLNGVEI/TRAVAACA	LRHLR--P--RELEAD	PLEITRKAAGPYKIK	TPOGAGHERRREKIV	372
E. coli	POEVAFPIAKRLRSN	IRELEGALTRIVANA	PNTPGRAITIDPVREA	LRDLA--A--LQEKVL	IDNIQVITVAYPYKIK	VADLAKRRERREKIV	372
T. mar.	PEEVLFNFAENVDDN	LRRLGAILIKLVYK	BTYGEVLDLKEAILL	LKDFIKPNRVKAMPD	IDELIETVAKVQVCP	REILNSRNV--KAL	372
H. pyl.	PEEVMEYIAQHSIDN	IRQMEGAIKISVNA	MLNANSIDNLAKTV	LEDL--QKDHAGSS	LENLILAVASLNLK	SSEIKVSSRQK--NVA	380
P. mar.	QARQVGMYLMRQGTN	LSLPRIGDTFGGKDH	TTVMYAIQVEKKLS	S-----DPQIA	SOVQKIRDLLQIDSR	RKR-----	461
Syn. sp.	LARQVGMYLMRQHTD	LSLPRIGEAFGGKDH	TTVMYSCDKITQLQ	-----DWETS	QTLTSLSHRINIAQ	APES-----	447
B. sut.	FRQIYAMLYSREMTD	SSLPGQIEEFGGRDH	TTVIHAHEIKSKLLA	D-----DEQLQ	GHEKVEIKBQLK----	-----	446
M. tub.	QSRQIYAMLYCRELTD	LSLPGIKQAQF--RDH	TTVMYAKRILSEMA	E-----DRREV	DHVKELTTRIRGRSK	R-----	507
T. th.	LPRLQIYAMLYVRELT	ASLPEITGQLPGGRDH	TTVRYAIQVQVQLAG	KP-----DREVQ	GLFRNTSLCTDTPWD	NLWITGC-----	446
E. coli	PRQAMALAKELTN	LSLPEIGDAQGRDH	TTVLHACRKBOLRE	E-----SHDIK	EDDETILRIATSS--	-----	467
T. mar.	TARRIGMYVAKYIKL	SSLRTIAEKN--RSH	PVVVDSVKKVDSLL	KG-----NKQLK	ALIDEVIGETISRRAL	SG-----	440
H. pyl.	LARKLVVVFARLYTP	NPTLSLAQFLDLKDH	SSISKSPVLSLREIK	-----	NRLNELNDKKTAFNS	SE-----	457

Figure 19

A)

GTGTGCGACGAGGCCGTCTGGCAACACGTTCTGGAGCACAC
 TCCGCCGCGAGCATCACCGAGGTGGAGTTCCACACCTGGTT
 TGAAAGGATCCGCCCTTGGGGATCCGGGACGGGGTGCTG 120
 GAGCTCGCCGTGCCACCTCCTTTGCCCTGGACTGGATCC
 GCGCCACTACGCGGCCCTCATCCAGGAGGGCCCTCGGCT
 CCTCGGGGCCAGGCGCCCGGTTGAGCTCCGGGTGGTG 240
 CCGGGGTCGTAGTCCAGGAGACATCTTCCAGCCCCCGC
 CGAGCCCCCGGCCAAGCTCAACCGAAGATACCTTAA
 AACTTCGTGGTGGGGCCCAACAATCCATGGGCCCAACGGC 360
 GCGCCGTGGCCGTGGCCGAGTCCCCCGCCGGCCCTACA
 ACCCCCTCTTCACTATACGGGGCGGTGGCTGGGAAAGAC
 CTACCTGATGCACGCCGTGGGCCACTCCGTGCGAAGCGC 480
 TCCCCCACATGAGATTAGAGTACGTTTCCACGAAACTT
 TCACCAACGAGCTCATCAACCGGCCATCCGCGAGGACCG
 GATGACGGAGTTCGGGAGCGGTACCGCTCCGTGGACCTC 600
 CTGCTGGTGGACGCTCCAGTTTCATCGCGGAAAGGAGC
 GCACCCAGGAGGATTTTCCACACCTTCAACGCCCTTTA
 CGAGGCCACAAAGCAGATCATCTCTCTCCGACCGGCCG 720
 CCCAAGGACATCTCACCTCGGAGCGCCTGCGGAGCC
 GCTTTGAGTGGGGCTGATCACCACAAATCCAGCCCCGA
 CCTGGAACCCGGATCGCCATCTTGAAGATGAACGCCAGC 840
 AGCGGCCCTGAGGATCCCGAGGACGCCCTGGAGTACATCG
 CCGCGCAGGTCACTCCAACATCCGGGAGTGGGAAGGGGC
 CCTCATCGCGGCATCGCCTTTTCGCCTCCCTCAACGGCGTT 960
 GAGCTGACCCGCGCGGTGGCGGCCAAGGCTCTCCGACATC
 TTCGCCCCAGGAGCTGGAGGCGGACCCCTTGAGATCAT
 CCGCAAAAGCGGGGACAGTTCGGCTGAAACCCCGGGA 1080
 GGAGCTCACGGGAGCGCCGCAAGAAGGAGGTGGTCTCTC
 CCGGCAGCTCGCATGTACCTGGTGGCGGAGCTACACCC
 GGCCTCCCTGCGCGAGATCGACAGCTCAACGACGACCGG 1200
 GACCACACACGGTCTCTACGCCATCCAGAAAGTCCAGG
 AGCTCGCGGAAAGCGACCGGGAGGTGAGGGCTCTCTCCG
 CACCTCCGGGAGCGGTGCACATGA

B)

VSHEAVWQHVLHIRRSITEVEFHTWFERIRPLGIRDGVL
 ELAVPTSFALDWIRRHAYGLIQEGRLLGAQAPRFELRVV
 PGVVQEDIFQPPSPPAQAQPEDTFKTSWWGPTTPWPHG 120
 GAVAVAESPGRAYNPLFIYGRGLGKTYLMHAVGPLRAKR
 FPHMRLEYVSTETFTNELINRPSARDMTEFRERYRVDL
 LLVDDVQFIAGKERTQEEFFHTFNALYEAHQIILSSDRP 240
 PKDILTLEARLRSRFEWGLITDNPADPLETRIAILKMNAS
 SGPEDEDALEYIARQVTSNIREWEGALMRASPFASLNGV
 ELTRAFAAKALRHLRPRELEADPLEIRKAAGPVRPETPG 360
 GAHGERRRKEVVLPRQLAMYLVRLELTPASLPEIDQLNDR
 DHTTVLYAIQKVQELAESDREVQGLLRLTREACT

Figure 20

A)

ATGAACATAACGGTTCCCAAAAACTCCTCTCGGACCAGC 40
 TTTCCCTCCTGGAGCGCATCGTCCCTCTAGAAGCGCCAA
 CCCCCTCTACACCTACCTGGGGCTTTACGCCGAGGAAGGG 120
 GCCTTGATCCTCTTCGGGACCAACGGGGAGGTGGACCTCG
 AGGTCCGCCCTCCCGCCGAGGCCCAAGCCTTCCCCGGGT 200
 GCTCGTCCCGGCCAGCCCTTCTTCCAGCTGGTGGGAGC
 CTCTCTGGGACCTCTGTGGCCCTCGGCCCTCGCCTCGGAGC 280
 CGGGCCAGGGGGGCGAGCTGGAGCTCTCCTCGGGCGTTT
 CCGCACCCGGCTCAGCCTGGCCCTGCCGAGGGCTACCCC 360
 GAGCTTCTGGTGCCCGAGGGGAGGACAAGGGGGCCTTCC
 CCTCCGGAGCGGGATGCCCTCCGGGGAGCTCGTCAAGGC 440
 CTTGACCCACGTGCGCTACGCCCGGAGCAACGAGGAGTAC
 CGGGCCATCTTCCGGGGGGTGAGCTGGAGTTCTCCCCC 520
 AGGGCTTCCGGGGCGTGGCCTCGAGCGGTACCGCCTCGC
 CCTCTACGACCTGCCCTTGCCCCAAGGGTTCCAGGCCAAG 600
 GCCGTGTCCCCGCCGAGCGTGGACGAGATGGTGGGG
 TCCTGAAGGGGCGGACGGGGCCGAGGCCGTCTCGCCCT 680
 GGGCGAGGGGGTGTGGCCCTGGCCCTCGAGGGCGGAAGC
 GGGTCCGGATGGCCCTCCGCCCTCATGGAAGGGAGTTCC 760
 CCGACTACCAAGGGTCATCCCCAGGAGTTCCGCCCTCAA
 GGTCAGGTGGAGGGGAGGCCCTCAGGGAGGCGGTGCGC 840
 CGGGTAGCGCTCTCTCCGACCGGAGAACCCCGGGTGG
 ACCTCCTTTTGAGGAAGGCCGATCCTCCTCTCCGCCGA 920
 GGGGACTACGGCAAGGGCAGGAGGAGGTGCCCGCCAG
 GTGGAGGGGCCGACATGGCCGTGGCCTACAACGCCCGCT 1000
 ACCTCCTCAGGACCTCGCCCGCGGGGACCGGGCCCA
 CCTGGGCTCTCCGGGCCACGAGCCCGAGCCTCATCTGG 1080
 GGGGACGGGAGGGGTACCGGGCGGTGGTGGTCCCTCA
 GGGTCTAG 1128

B)

MNITVPKLLSDQLSLERIVPSRSANPLYTYLGLYAEEG 40
 ALILFCTNGEVDLEVRLPAAQSLPRVLVPAQFFQLVRS
 LPGDLVALGLASEPQGQGLLESSGRFRTRLSLAPAEQYP 120
 ELLVPEGEDKGAFFLRTRMPGSELVKALTHVRYAASNEEY
 RAIFRGVQLFESPQGFRAVADGYRLALYDLPLPQGFQAK 200
 AVVPARSVDENVRLKGADGAEAVLALGEGVLALALEGGS
 GVRMALRLMEGEFPDYQRVIPQEFALKVQVEGEALREAVR 280
 RVSVLSDRQNHRVDLLLEGRILLSAEGDYGKGQEEVPAQ
 VEGPDMAVAYNARYLLEALAPVGDRALHGTSGTPSPSLIW 360
 GDGEGYRAVVVPLRVZ

Figure 21

T.th.beta MNITVPKKLLSDQLSLERIVPSRSANPLYTYLGLYAEAGAILFOTNGEVDLEVRPAE
E.coli.bet MKPTVEREHLKFLQGVSGPLQGRPTLPILGNLLQVADGTLSTLTQLEMMARVALV
P.mirab.be MKFIIEBQLKFLQGVSGPLQGRPTLPILGNLLKVIENTLSLTQLEMMARVSL
H.infl.bet MQFSISRENLLKFLQGVSGVLSNRNPTPLVNLNVLQIEDYRLTITGTDLEVELSSQTQLS
P.put.beta MHFTIQREALLKFLQGVAGVVERRTLPVLSNVLVVGQQLSLATGTDLEVELVGROLE
B.cap.beta MKFTIQNDILTKNLAKITRVLVKNSPPILENILIQVEDGTLSTLTNNLEIELISKIETI
* * * * *

T.th.beta AQSLP-RVLVPAQPFQVRLSGDLVALGLASEPQGGQLELSSGRFFRLTSLAPAEY
E.coli.bet QSHFGATTVPARKFFDICRGLP-EGAEIAVQLE---GERMLVRSGRSRLSTLPAADF
P.mirab.be QSHFGATTVPARKFFDIWRGLP-EGAEISVELD---GDRLLVRSGRSRLSTLPAADF
H.infl.bet SSENKOTFTTPAKFKLDICRTLSDSEITVTFE---QDRALVQSGRGRPTLSTQPAEY
P.put.beta EPAEPGEITVPARKLMDICKSLP-NDALIDIKVD---EQKLLVRSGRSRLSTLPAADF
B.cap.beta TKYIPGKTTISGRKILNICRTLSEKSKIMQLK---NKGWVSSSENNTLSTLSADTF
* * * * *

T.th.beta PELLVPEGEDKGAFFLRTMPSGELVKALTHVRYAASNEEYRAIPRGQVLEFSPQGFRAV
E.coli.bet PNLDD--WQSEVEFTLPQAT---MKRLIEATQFSMAHQDVRYLAKMLFETEGEELRTV
P.mirab.be PNLDD--WQSEVEFTLPQAT---LKRLIESTQFSMAHQDVRYLAKMLFETENTELRTV
H.infl.bet PNLTD--WQSEVDFELPQAT---LRLLEATQFSMAHQDARYFLKMKFETEGNLLRTV
P.put.beta PTVEE--GPGSLTCLNLEQSK---LRLIERTSFAMAQDVRYLAKMLLEFVSRNTLRV
B.cap.beta PNHNQ--FDYISKFDISSNI---LKEMIEKTEFSMKQDVRYLAKMLLEKKDKFLRSV
* * * * *

T.th.beta ASDGYRLALYDLPLQGFQA--KAVVPARSVDDEM/RVLKGADGAEVALGEGVLALAE
E.coli.bet ATDGHRLAVCSMPIGQSLPS-HSVIVPRKGVIELMRMLDG-GDNLPRVQIGSNINRAHV
P.mirab.be ATDGHRLAVCAMDIGQSLPG-HSVIVPRKGVIELMRMLDGSGESLQIQIGSNINRAHV
H.infl.bet ATDGHRLAVCTISLQELQN-HSVILPRKGVIELMRMLLET-NDEPARLQIGTNINRAHVK
P.put.beta STDGHRLALCSMAPIEQEDRHQVIVPRKGVILELRLTLD-PEGMVSVLQGHIRATTC
B.cap.beta ATDGYRLAISYTLQKKDINF-PSIIIPKAVMMLKLLINT-QPQLNLLIGNSIRIYTK
..** *** ..* * * *

T.th.beta GSGVFMALRLMEGEFPDYQVRVLPQEFALKVQVEGALREALRVRSVLSDRQNHVDLL
E.coli.bet ---DFIPTSCLVDGRFPDYRRVLPKNPDKLEAGCDLLKQAFARAAILSNEKFRGVRLV
P.mirab.be ---DFIPTSCLVDGRFPDYRRVLPKNPTKTIVLAGCDILKQAFARAAILSNEKFRGVRLN
H.infl.bet ---NTVFTSKLIDGRFPDYRRVLPKNPNATKIVGNGWMLKQAFARASILSNERARSVRLSL
P.put.beta ---EFTFTSKLVDGRFPDYRRVLPKGGDKLVVGDQALREAFSRTAILSNEKFRGRLQL
B.cap.beta ---NLIFTTLQIEGEYPDYKSVLFKEKNPIITNSILLKSLRLVAILAHEKFCGIEIKI
* * * * *

T.th.beta BEGRILLSAEGDYGK-GQEEVPAQVEGPDMAVYNNARYLLEALAPVG-DRAHLIGISPTS
E.coli.bet SENQLKITANNPQEEAEIILDVYSGAEMELGFNVSYLLDVNLALKCEVNRMLTDSVS
P.mirab.be TNGQLKITANNPQEEAEIILDVYSGAEMELGFNVSYLLDVNLALKCEVNRMLTDAVS
H.infl.bet KENQLKITASNTPEEAEIILDVYNGEELVGFNVTYILDLNLALKCNQVRMLCTDAFS
P.put.beta AAGQLKITANNPQEEAEIISVDYEGSSLEIGFNVSYLLDVNLVMTTEQVRLILSDNS
B.cap.beta ENGKFKVLSNQEEETAEDLFEIDYFGEKIEISINVYLLDVINNKSENKAILNFKSKS
* * * * *

T.th.beta PSLIWGDG-EGYRAVVVPLRVZ (ID#108)
E.coli.bet SVQIEDAASQAAVVMPMRLZ (ID#109)
P.mirab.be SVQVENVASAAAAYVMPMRL (ID#110)
H.infl.bet SCLIENCEDSSCEYVMPMRL (ID#111)
P.put.beta SALLQEGNDDSSVVMPMRL (ID#112)
B.cap.beta SIQTEAENNSNAYVMLLKR- (ID#113)
* * * * *

Figure 22

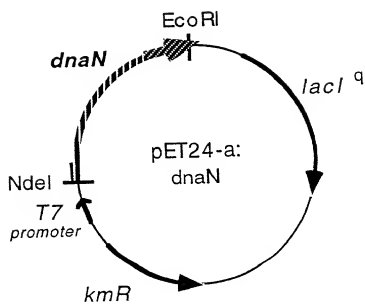
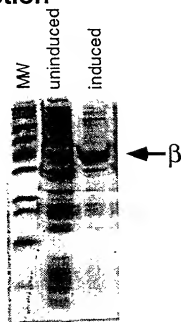


Figure 23

A) Induction

↓
Lysis
↓
Heat Step
↓

B) MonoQ Column

Fraction: 5 7 9 11 13 15 17 19 21 23 25

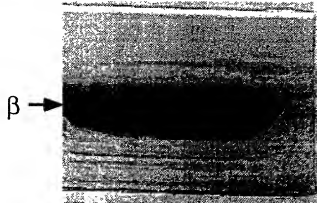


Figure 24

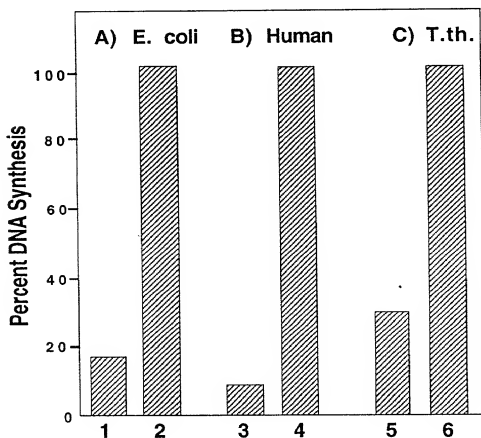
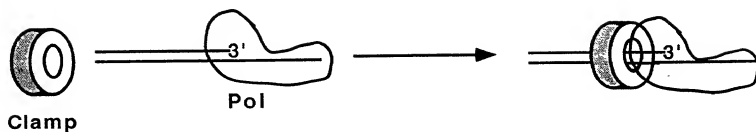


Figure 25

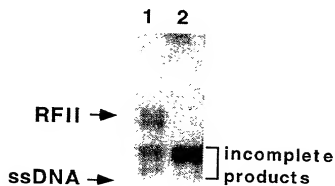
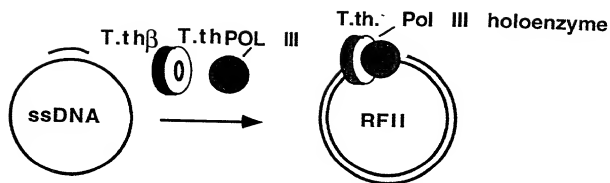


Figure 26